What is claimed is:

1. An isolated polynucleotide containing a polynucleotide sequence selected from the group consisting of

a) a polynucleotide which is at least 70% identical to a polynucleotide which encodes a polypeptide containing the amino acid sequence of SEQ ID no. 2,

b) a polynucleotide which encodes a polypeptide which contains an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID no. 2,

c) a polynucleotide which is complementary to the polynucleotides of a) or b), and

d) a polynucleotide containing at least 15 successive nucleotides of the polynucleotide sequences of a), b) or c).

2. The polynucleotide according to claim 1, wherein the polynucleotide is a preferably recombinant DNA replicable in coryneform bacteria.

3. The polynucleotide according to claim 1, wherein the polynucleotide is an RNA.

4. The polynucleotide according to claim 2, containing the nucleic acid sequence as shown in SEQ ID no. 1.

5. The polynucleotide according to claim 2 that is a replicable DNA containing

(i) the nucleotide sequence shown in SEQ ID no. 1, or

(ii) at least one sequence which matches the sequences (i) within the degeneration range of the genetic code, or

(iii) at least one sequence which hybridizes with the complementary sequences to sequences (i) or (ii) and optionally

(iv) functionally neutral sense mutations in (i).

6. A vector containing the polynucleotide according to claim 1, in particular pXT-dapCexp, which is characterized by the restriction map shown in Figure 2, deposited under the designation DSM 13254 in Corynebacterium glutamicum.

7. Coryneform bacteria acting as host cell which contain the vector according to claim 6 or in which the zwa1 gene is enhanced.

8. A process for the production of L-amino acids, in particular L-lysine, wherein the following steps are performed:

a) fermentation of the bacteria producing the desired L-amino acid bacteria, in which at least the dapC gene is enhanced,

b) accumulation of the desired product in the medium or in the cells of the bacteria, and

c) isolation of the L-amino acid.

9. The process according to claim 8, wherein the bacteria are used in which further genes of the biosynthetic pathway of the desired L-amino acid are additionally enhanced.

10. The process according to claim 8, wherein the bacteria are used in which the metabolic pathways which reduce the formation of L-lysine are at least partially suppressed.

11. The process according to claim 8, wherein coryneform bacteria are used which produce L-lysine.

12. The process according to claim 8, wherein the bacteria are fermented for the production of L-lysine, in which, in addition to the dapC gene, one or more genes selected from the group consisting of

12.1 the lysC gene, which encodes a feed back resistant aspartate kinase,

12.2 the asd gene, which encodes aspartate semialdehyde dehydrogenase,

12.3 the dapA gene, which encodes dihydropicolinate synthase,

12.4 the dapB gene, which encodes dihydrodipicolinate reductase,

12.5 the dapD gene, which encodes tetrahydropicolinate succinylase,

12.6 the dapE gene, which encodes N-succinyldiaminopimelate desuccinylase,

12.7 the dapF gene, which encodes diaminopimelate epimerase,

12.8 the lysA gene, which encodes diaminopimelate decarboxylase,

12.9 the ddh gene, which encodes diaminopimelate dehydrogenase,

12.10 the lysE gene, which encodes lysine export,

12.11 the pyc gene, which encodes pyruvate carboxylase,

12.12 the mqo gene, which encodes malate:quinone oxidoreductase,

12.13 the zwa1 gene

12.14 the gdh gene, which encodes glutamate dehydrogenase,

are simultaneously enhanced, over-expressed or amplified.

13. The process according to claim 8, wherein the bacteria are fermented for the production of L-lysine in which one or more of the genes selected from the group consisting of

13.1 the pck gene, which encodes phosphoenolpyruvate carboxykinase,

13.2 the pgi gene, which encodes glucose 6-phosphate isomerase,

13.3 the poxB gene, which encodes pyruvate oxidase,

13.4 the zwa2 gene,

13.5 the sucC or sucD genes, which encode succinyl CoA synthetase

is/are simultaneously attenuated.

14. A process according to one of claims 8-13, wherein microorganisms of the genus Corynebacterium glutamicum are used.

15. A hybridization probe comprising a polynucleotide sequence according to claim 1.

16. A method for isolating cDNA which encodes the product of the dapC gene comprising contacting the hybridization probe of claim 15 with a sample.

17. A method for isolation of cDNA or genes which exhibit a high level of similarity with the sequence of the dapC gene comprising contacting a hybridization probe according to claim 15 with a sample.

18. DNA originating from coryneform bacteria which encodes N-succinylaminoketopimelate transaminase, in which the amino acid sequence shown in SEQ ID no. 2 in position 209 is replaced with another amino acid, with the exception of L-proline.

19. DNA according to claim 18, wherein the amino acid L-proline in position 209 of the enzyme protein (SEQ ID no. 2) is replaced with L-leucine (SEQ ID no. 4).

20. DNA according to claim 18, wherein the replacement of L-proline with L-leucine in position 209 is effected by the replacement of the nucleobase cytosine in position 716 with thymine, as shown in SEQ ID no. 3.

21. Coryneform bacteria which contain DNA according to claim 17, 18 or 19.